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GENOME ANNOUNCEMENT

Genome Sequence of *Fibrella aestuarina* BUZ 2^T, a Filamentous Marine Bacterium

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***Fibrella aestuarina* BUZ 2^T is the type strain of the recently characterized genus *Fibrella*. Here we report the draft genome sequence of this strain, which consists of a single scaffold representing the chromosome (with 11 gaps) and a 161-kb circular plasmid.**

Fibrella aestuarina BUZ 2^T is the type strain of the genus *Fibrella*, which was characterized in 2011 (1). The organism was isolated from coastal mud from the North Sea (Fedderwardersiel, Germany). It belongs to the *Cytophagaceae* family in the *Bacteroidetes* phylum. This bacterium forms multicellular filaments (chains of cells) during growth and has pink pigmentation. We sequenced the genome of *F. aestuarina* to learn more about the biology of this organism and for comparative studies with other sequenced members of the phylum.

Bacteria were grown overnight in SM broth (DSMZ medium 7) at 28°C. DNA was isolated using the Genomic 500 DNA kit (Qiagen, Hilden, Germany) following the instructions of the manufacturer. The cell lysis modification and prolonged incubation time used for *Spirosoma linguale* (2) were applied for this bacterium, based on its phylogenetic relationship.

The genome was sequenced at the Functional Genomics Center Zurich (Zurich, Switzerland) with Roche 454 GS FLX Titanium chemistry. Two libraries were prepared: half a plate with an 8-kb insert paired-end library and half a plate with a shotgun library. This strategy yielded a total of 1,539,188 reads with an average size of 410 nucleotides. Assembly was done using the GS DeNovo Assembler version 2.5.3 (Roche) with various parameter settings. The two best assemblies were merged using Minimus 2 version 3.00 (5) and scaffolded using Oslay software version 1.0 (4). The assembly was further improved by mapping the pair-end reads against the assembly and manually checking the gap regions, which allowed the closure of most gaps. The final genome sequence of *F. aestuarina* is composed of two sequences: a scaffold representing the chromosome with 11 gaps, and a plasmid (pFAES01). The total chromosome size is 6,775,444 bp, with a total of 11 gaps and 8,105 ambiguous bases; the G+C content is 56.5%. The total size of the circular plasmid is 161,819 bp, with a G+C content of 52.7%. The average coverage for the chromosome was 63.3-fold, and that for the plasmid was 83.4-fold.

The GenDB annotation platform (3) was employed for the genome annotation. A total of 5,480 protein-coding sequences (CDSs) and 76 structural RNAs (67 tRNAs and 9 rRNAs) on the chromosome and 147 CDSs on the plasmid (pFAES01) were annotated.

The sequencing of more genomes of filamentous bacteria will allow the identification of genes responsible for filamentation and therefore provide some indications regarding the evolution of multicellularity in bacteria. A comprehensive comparative genome analysis with neighbor genomes is under way.

Nucleotide sequence accession numbers. The genome sequence has been deposited at EBI under the accession number HE796683 for the chromosome and accession number HE796684 for the plasmid.

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